GENETIC PROFILE OF EXTENDED-SPECTRUM B-LACTAMASE PRODUCING ENTEROBACTERIACEAE ISOLATED FROM BLOODSTREAM INFECTIONS IN A PUBLIC HOSPITAL IN SALVADOR, BAHIA.

Authors Leal, H.F ², Freire, L.B ¹, Menezes, A.P ³, Roma, L. R. C.¹, Amorim, A M.L.¹, Barros, T.F ¹; Reis, J.N.¹

Institutions

¹ UFBA – Universidade Federal da Bahia, Faculdade de Farmácia (Rua Barão do Jeremoabo, n° 147, Ondina - Salvador, Bahia - Brasil, 40.170-115), ² FIOCRUZ – Fundação Oswaldo Cruz, Centro de Pesquisas Gonçalo Moniz (R. Waldemar Falcão, 121 - Candeal, Salvador - BA, 40296-710), ³ UESB-Universidade Estadual do Sudoeste da Bahia (Rua José Moreira Sobrinho, s/n – Jequiézinho Jequié –BA – 45200-000).

Abstract:

Multiresistant bacteria have been emerged and spread extremely fast all over the world, already being known as a public health issue, since it increases the costs of hospitalization; the patient's length of stay in hospital and reduce therapeutic options. Moreover, infections caused by these bacteria have been associated with high mortality rates since these microorganisms are known to induce a strong immune response in the host and are widely associated with resistance mechanisms. The aim of this study was to characterize the most important ESBL and carbapenemases encoding genes of enterobacteriaceae isolated from bloodstream infections from May 2013 to April 2014 in a public hospital of Salvador, Bahia. A total of 44 ESBL phenotypically positive enterobacteria isolates were analyzed by three Multiplex PCR, in order to identify the presence of TEM genes (TEM-1 and TEM-2), SHV and OXA-1like (OXA-1, OXA-4 e OXA-30), CTX-M-group 1, CTX-M-group 2 and CTX-M-group 9 - ESBL encoding genes - and IMP, VIM and KPC, those which encode carbapenemases. A total of 25 isolates (56%) were identified as K.pneumoniae; 9 (20%) E.cloacae; 3 (6,8%) were either S.marcecens and E.coli and 1 sample (4,4%) of P.mirabilis, M.morganii, C.freudii e K.oxytoca, each. Just 2 samples did not present any of the studied resistance genes. The most found genes were: OXA (71,4%) CTX-M-1 (64,3%), SHV (50%), TEM (45%), CTX-M-2 (21,4%), e CTX-M-9 (2,4%). The presence of more than one resistance gene was identified in 32 isolates and 3 isolates showed carbapenems resistance genes. The KPC gene was identified only in an isolated, which was resistant to carbapenems and the IMP gene was identified in two isolates sensitive to that antibiotic. These epidemiological findings demonstrate that, indeed, multiresistant bacteria are widespread in the hospital environment and these informations can act as a guide, directing the appropriate treatment of infections caused by these microrganisms.

Key-words: enterobacteria, multiresistant, MDR, Multiplex, ESBL, carabapemases, bloodstream infections.

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